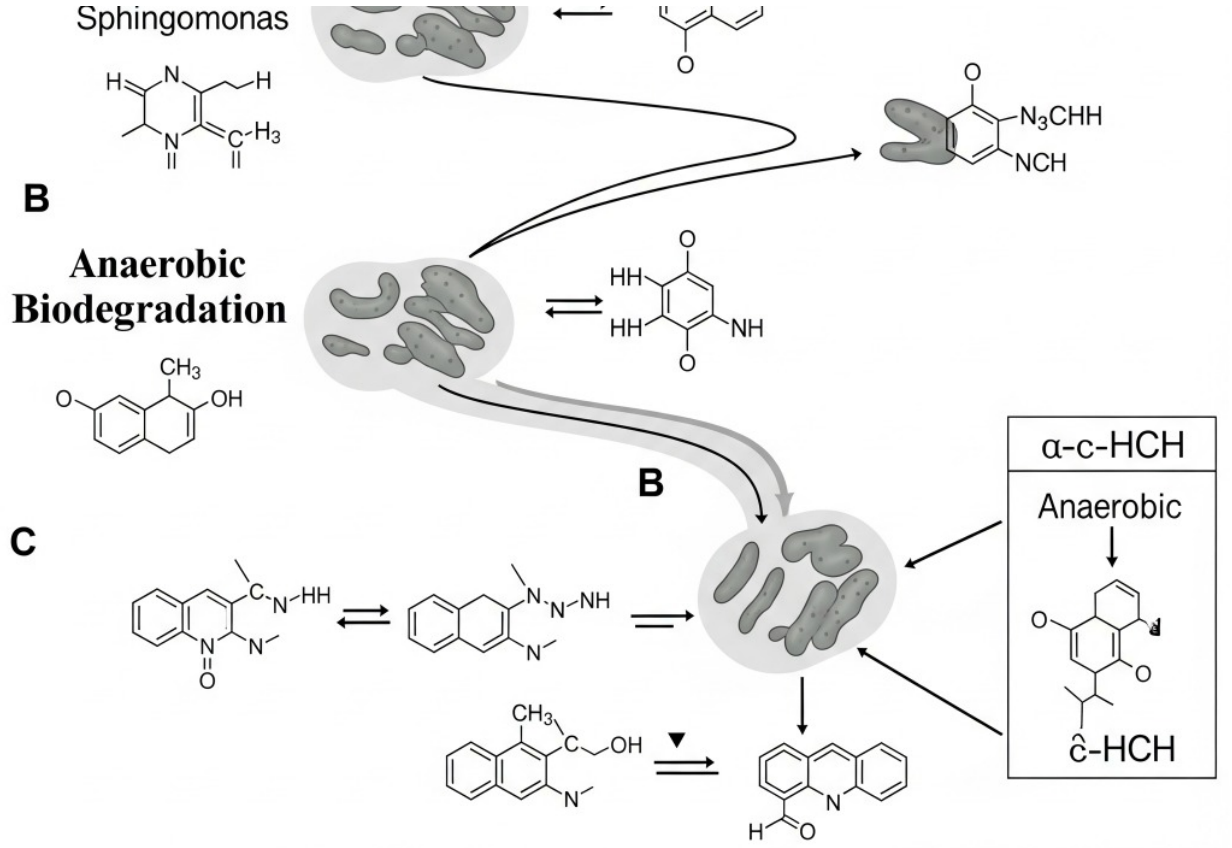
Biodegradation of HCH Isomers by Soil Bacteria



	Bacterial species	
Sphingomonas	c-HCH	Prefered HCH isovity

Biodegradation of HCH Isomers by Soil Bacteria: Mechanisms and Microbial Diversity

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Introduction

An introduction to "Biodegradation of HCH Isomers by Soil Bacteria" Hexachlorocyclohexane (HCH) and its isomers have posed a significant challenge to environmental health due to their persistence and toxicity. Despite their hazardous nature, a range of bacterial strains—both aerobic and anaerobic—have shown the ability to degrade these pollutants.

Understanding the mechanisms of microbial degradation and the specific strains involved is crucial for developing effective bioremediation strategies. This section of the thesis details the microbial species known to degrade HCH, outlines their metabolic pathways, and discusses the microbial diversity found at contaminated sites.

The information presented is highly relevant for environmental microbiologists, researchers in bioremediation, and students studying soil microbiology and pollutant degradation. The focus keyword *biodegradation of HCH* is included early for SEO optimization.

> ## *Microbial Mechanisms for the Biodegradation of HCH*
>
> ***1.3. HCH biodegradation***
> *Despite of the fact that HCH isomers are highly toxic and persist in the environment, HCH is still biodegradable by a group of micro-organisms (Lal et al., 2010). Both anaerobic and aerobic types of degradation have been identified. Few fungi are also reported to degrade δ isomer of HCH (Tu, 1976).*
>
> *Anaerobic degradation (MacCrae et al., 1969; Jagnow et al., 1977) has been observed by isolates belonging to the genera Clostridium, Citrobacter, Desulfovibrio, Desulfococcus, Dehalobacter etc. While aerobic degradation is mainly contributed by members of aerobic Proteobacteria from the family Sphingomonadaceae (Lal et al., 2008) out of which three strains, previously denoted as Sphingomonas paucimobilis have been extensively studied for HCH degradation.*

These were isolated from different geographical locations like Japan (S. japonicum UT26) Seno & Wada, 1989; India (S. indicum B90A) Sahu et al., 1990 and France (S. francense Sp+) Cérémonie et al., 2006. However, bacteria belonging to other genera have also been studied for their role in HCH degradation (Table 2.1).

Table 2.1: List of few HCH degrading bacteria isolated from different geographical regions of the world.

See in orignal thesis

Detailed aerobic degradation pathway of γ-HCH has been studied in S. japonicum UT26, but it is not able to completely mineralize other isomers, especially, the β- and δ-HCH. Sphingobium indicum B90A (Kumari et al., 2002) which was initially isolated from rice rhizosphere soil in India, is known to aerobically transform all HCH isomers including the most recalcitrant β-HCH (Lal et al., 2010).

The HCH degrading aerobic bacteria possess lin genes which are known to degrade HCH (Nagata et al., 1999). The lin gene sequences and organization are almost identical with a few exceptions irrespective of the fact that they belong to different genera. The lin system has evolved for HCH degradation, making it interesting to study evolutionary metabolic pathways.

This slight difference in the gene organization (Sharma et al., 2006) is the reason that these bacteria exhibit variation in the degradation of HCH isomers (Lal et al., 2010).

Microbial Diversity at HCH Contaminated Sites

1.4. Microbial diversity at HCH contaminated sites

As already known, diverse HCH degrading bacteria have been isolated from different parts of the world while, very few reports are available on the microbial communities at the HCH contaminated sites.

In 2005, Böltner et al. isolated a few bacterial species using culturable approach after enrichment of HCH contaminated soil from Chemnitz, Germany. All the isolated strains belonged to the genus Sphingomonas.

Microarray-based detection technique has also been used to assess the microbial diversity from HCH contaminated soil in Spain and the results exhibited predominant signals for the presence Sphingomonas species (Neufeld et al., 2006). Another study addressed this issue by isolating bacteria from 13 soil samples, varying in levels of HCH contamination, from four sites in Spain (Mohn et al., 2006).

Nine HCH degrading isolates were obtained, all belonging to the genus Sphingomonas. Dadhwal et al. (2009) isolated 24 bacterial strains from HCH contaminated soils (maximum 32 mg g^{-1} of soil) from the HCH dumpsite, Ummari village, Lucknow, India. Some of the isolated strains were found to be efficient degraders of HCH isomers (α-, γ-, β-, and δ-HCH) even better than S. indicum B90A.

In concurrence with previous studies, majority of the isolates obtained were members of the genus Sphingomonas, suggesting that they are one of most readily isolated group from HCH contaminated sites and has been extensively studied for HCH degradation (Lal et al., 2010).

Recently, Manickam et al. (2010) reported the soil community of the soil sample collected from the vicinity of IPL (India Pesticides Limited), Chinhat, Lucknow, that majorly consisted of uncultured environmental clones and also revealed the presence of Sphingomonas, Pseudomonas etc. The waste isomers produced from the IPL have been deposited at HCH dumpsite during the past 10 years.

This site is located in Ummari village, Barabanki, Lucknow, which is 13 km away from the lindane manufacturing unit (Jit et al., 2011).

Microbial community analyses of this site (Lal, 2011) using cloning and T-RFLP of 16S rRNA gene indicated the presence of Chromohalobacter, Alcanivorax, Pseudomonas, Marinobacter, Halomonas, Bordetella, Clostridium, Mycobacterium, Escherichia and sphingomonads.

Thus, few reports exist on the diversity of HCH contaminated sites and there is scarce knowledge on organisms responsible for any adaptation of soil communities to HCH contamination.

Therefore, for the requirement for novel HCH degrading strains, studying

> *the microbial diversity at these sites can be an initial step.*

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